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Performance of Copan WASP for Routine Urine Microbiology

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Abstract

This study compared manual workup of urine clinical samples with fully automated WASPLab processing. As a first step two different inocula (1 and 10 µl) and different streaking patterns were compared using WASP and InoqulA BT™ instrumentation. A 10 µl inoculum produced significantly more single colonies than a 1 µl inoculum and automated streaking yielded significantly more single colonies as compared to manual streaking on whole plates ($p<0.001$). In a second step, 379 clinical urine samples were evaluated using WASP and manual workup. Average numbers of detected morphologies, recovered species, and CFU/ml of all 379 urine samples showed excellent agreement of WASPLab and manual workup. The percentage of clinical categorization of urine samples as "positive" or "negative" did not differ between automated and manual work-flow but within the positive samples automated processing by WASPLab resulted in the detection of more potential pathogens. In summary, the present study demonstrates that i) the streaking pattern, i.e. primarily the number of zigzags/length of streaking lines, is critical for optimizing the number of single colonies yielded from primary cultures of urine samples, ii) automated streaking by the WASP instrument was superior to manual streaking regarding the number of single colonies yielded, (for 32.2%) iii) automated streaking leads to higher numbers of detected morphologies (for 47.5%), species (for 17.4%) and pathogens (for 3.4%). The results of this study point to an improved quality of microbiological analyses and laboratory reports when using automated sample processing by WASP and WASPLab.

Introduction

In recent years, clinical microbiology has been faced with dramatic changes, as full laboratory automation (FLA) has started to enter diagnostic laboratories. This trend to automation will affect to various extents economic efficiency, standardization, and time-to-result of laboratory procedures (16). To date, clinical microbiology is still predominately based on manual sample processing. Compared to clinical chemistry, microbiological specimens display a significantly higher degree of complexity (2). Thus, for many years the general perception was that clinical microbiology would be far too complex to allow for automated processing, and that robots would not be able to replace human operators. However, it has been demonstrated that automated inoculation of samples can be superior to manual processing and that automated reading of disk diffusion agar plates significantly increases precision of results (4, 5, 9, 13). Thus, automated sample processing promises an improved standardization of sample processing, incubation times, and plate reading protocols.

FLA systems have been developed by several companies. Currently, there are two FLA solutions available, i.e. BD Kiestra total laboratory automation (TLA™; BD Kiestra B.V., Drachten, Netherlands) and WASPLab (Copan Italia S.p.A., Brescia, Italy). These systems use robotic systems for handling specimen containers and primary culture inoculation specifically the Kiestra InoqulA and the Copan WASP. The inoculated media are moved to automated incubators by conveyor belts with integrated camera systems to capture plate images at given time points which is henceforth referred to in this article as WASPLab. Currently, digital plate reading (DPR) is still depending on highly skilled technologists, who can read plates “virtually” without

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66 physical interaction (15). First studies on FLA solutions suggest that productivity
67 indicators can be improved and diagnostic processes can be accelerated (3, 6, 7, 14).
68 In the present study, we compared workflows for urine sample processing using
69 the fully automated WASP and WASPLab systems and manual standard procedures.
70 Inoculation procedures critically influence further procedures such as specimen
71 identification (ID) and antimicrobial susceptibility testing (AST), mainly by the ability to
72 generate single colonies suitable for further processing. Therefore, both streaking
73 pattern and inoculation volume should be well evaluated prior to compare total manual
74 and automated workflows. Different guidelines exist for urine specimen inoculation, e.g.
75 U.S. and Canadian laboratories routinely plate 1 µl of urine specimens, whereas
76 European guidelines suggest 10 µl (5, 18). Therefore, this study was subdivided in two
77 parts: In part one, the ability to generate single colonies was compared for i) manual
78 and automated workflows and ii) for different automated streaking patterns using pure
79 and mixed cultures and different inocula (1 µl and 10 µl) in order to determine the
80 optimal streaking pattern. Part two of the present study compared total manual and
81 automated workflows regarding i) the number of detected CFU, ii) the number of
82 detected morphologies, iii) the number of recovered species, and iv) the number of
83 follow-up testing after initial plate reading, i.e. the number of identifications and
84 susceptibility tests, in 379 clinical urine samples.
85
86 **Materials and Methods**
87 **Bacterial strains, clinical samples and growth conditions.** Urine samples and
88 bacterial strains isolated from patient specimens used in this study were collected from

January until April 2015 in the clinical laboratory of the Institute of Medical Microbiology, University of Zurich. If not stated otherwise bacterial cultures were incubated at 35 °C ±2 °C and 7.5% CO_2 for 16h-20h.

Quantitative analysis of streaking pattern/single colony count. Manual, semi and fully automated quantitative streaking patterns were evaluated by counting the number of single colonies produced on whole plates. Manual streaking was always performed by the same investigator with a 1 µl and a 10 µl calibrated plastic inoculation loop (Copan Italia S.p.A., Brescia, Italy) resulting in 9-10 zigzag lines (Figure 3A). For the semi-automated streaking, a "ball-based" benchtop InoqulA BT™ (BD Kiestra, Drachten, Netherlands) was used with a 1 µl and 10 µl inoculum and the zigzag liquid streaking pattern resulting in 20 zigzag lines (Figure 3A). In this study, 1 µl and 10 µl inocula were manual pipetted for InoqulA BT. Furthermore, 1 µl was taken in consideration as per term of comparison but it has to be noted that the BD Kiestra solutions cannot handle 1 µl. The fully automated streaking was performed by the "loop-based" WASP (Copan Italia S.p.A.) with two different streaking patterns; the single streak type 2 (SST2, 11 zigzag lines) and the single streak type 6 (SST6, 27 zigzag lines, Figure 3A). Bacterial suspensions of McFarland 0.5, corresponding to ~1.5 x 10^8 colony forming units per ml (CFU/ml), were serial diluted in sodium borate/formate containing BD Vacutainer (BD, Franklin Lakes, NJ, USA) and plated onto Columbia 5 % sheep blood agar (COS, bioMérieux SA, Marcy l'Etoile, France) for monomicrobial cultures or chromogenic Uri*Select*™ 4 agar (URI4, Bio-Rad Laboratories, Hercules, CA, USA) for polymicrobial cultures. Pure *Escherichia coli* and enterococci cultures were diluted to 10^4-10^6 CFU/ml and mixed cultures were prepared with *E. coli* ranging from

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10^4 to 10^6 CFU/ml together with 10^6 enterococci and 10^6 coagulase negative staphylococci (CoNS). The single colony counting was done manually by eye by the same investigator.

Head to head comparison of urine samples. In total, 379 clinical urine samples were processed in parallel by the fully automated WASPLab (Copan Italia S.p.A.) workflow (inoculation, incubation, image acquisition, image analysis) and the manual routine procedures of our clinical laboratory. 1 µl sample inoculum used in the manual routine workflow was compared to 1 µl (121 samples) and 10 µl loop (379 samples) of the WASP. Urine cultures were plated onto COS, URI4 and Columbia colistin-nalidixic acid (CNA) agar 5 % sheep blood (bioMérieux SA).

Following manual inoculation agar plates were analyzed after one and two days of incubation and morphologies, CFU count, and recovered species were recorded. Material was reported negative when there was no growth or growth of a non-relevant pathogen after two days of incubation. Materials were reported positive, if there was a relevant pathogen in a relevant quantity, and if treatment was indicated. The sample evaluation algorithm used resembles the diagnostic approach as suggested by the Cumitech guidelines (12). Classification of the relevant pathogens was done as reported elsewhere (10).

For WASP inoculation, 1 µl and 10 µl volumes of the urine sample were streaked with the SST6 streaking pattern. Images were taken using WASPLab imaging after 16 and 38 h incubation at 35 °C ±2 °C and 7.5% CO_2 and analyzed by the same laboratory personnel. After 16 h photos were read, morphologies (i.e. visually different colony types), and CFU counts were noted. Plates were re-read after 38 h incubation. Colonies

with additional morphology were identified. Samples were categorized as negative and positive according to the same criteria as for the manual reading procedure. Besides the number of different morphologies, CFU counts and recovered species (i.e. taxonomic entities as reported by MALDI-TOF-MS identification), the number of follow-up tests, such as susceptibility tests and matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS, Bruker Daltonics, Bremen, Germany) identifications, were recorded for comparison.

Plate reading of manually examined specimens was performed by different laboratory personnel by visual inspection directly; plates of WASP-prepared samples were read by a single technician with the WASPLab, who also did the head-to-head comparison of the final dataset.

Technical settings of WASPLab. Automated images of COS and CNA plates were recorded using three different light settings (Top-light, Dark-field, and a combination of Top and Back-light). URI4 images were recorded with Top-light settings only. The WASPLab installation used WASPCore version 3.1.0. The settings were conserved throughout the whole study duration.

Statistical analysis. Statistical analysis was performed using the IBM SPSS statistic software, version 20 (SPSS Inc., Chicago, IL, USA). The normality of the data was assessed with the Kolmogorov-Smirnov and Shapiro-Wilk test, followed by the paired t-test and the non-parametric Wilcoxon signed rank test for the comparison of loop size and streaking pattern for pure cultures. A cutoff value of 0.05 was considered as statistically significant. For the mixed cultures, overall differences were tested using the Kruskal-Wallis and the one way ANOVA with Bonferroni post hoc test to control for

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alpha inflation. Non-parametric Follow-up tests were conducted using the Mann-Whitney U test for pairwise comparison with Bonferroni correction applied for multiple comparisons with an alpha level of 0.05 divided by possible number of comparisons i.e. 0.0083 (=0.05/6) for streaking pattern and 0.0167 (=0.05/3) for concentration as independent variables. To compare the proportion between manual and WASP processing of the head to head comparison the Wilcoxon signed rank test and a crosstab chi-square test of independence were performed. Proportions do differ significantly from each other at the level of 0.05.

Results

As a first step two different inocula (1 µl and 10 µl) and different streaking patterns (one manual, two fully automated WASP/"loop-based", and one semi-automated InoqulA/"ball-based") were evaluated with pure cultures of *E. coli* and enterococci using CFU counts of 10^4/ml, 10^5/ml, and 10^6/ml, with the view to identify the loop-streaking pattern combination which yields the highest number of single colonies isolated (Figure 2, Figures S1 and S2).

We also studied, mixed inocula containing 10^6 CFU/ml enterococci, 10^6 CFU/ml CoNS, and *E. coli* with CFU/ml ranging from 10^4 CFU/ml to 10^6 CFU/ml with the view to mimic mixed clinical samples of a leading pathogen and residual flora.

Evaluation of the optimal inoculation volume

The 10 µl inoculum produced significantly more single colonies than the 1 µl inoculum on whole plates for both *E. coli* and enterococci when using CFU counts between 10^4/ml and 10^5/ml. This finding was independent from the streaking pattern ($p<0.001$, Figure 2, B and C). In contrast, no significantly higher recovery of single colonies was observed for *E. coli* CFUs of 10^6/ml when using a 10 µl versus 1 µl inoculum and when comparing manual streaking and the InoqulA ($p=0.820$, and $p=0.713$, respectively) (Figure 2, B and C). However, WASP inoculation retained a significantly higher recovery of single colonies when applying the 10 µl inoculum ($p<0.001$, Figure 2, B and C) and manual streaking.

Analysis of mixed cultures of *E. coli*, enterococci, and CoNS basically resembled the results of pure cultures (Figure 3): The 10 µl inoculum resulted in the recovery of

188 significantly more single colonies than the 1 µl inoculum for manual streaking, WASP
189 SST6 and the InoqulA ($p<0.001$).

190 ***Evaluation of the optimal streaking pattern***

191 For pure cultures of *E. coli* and enterococci the WASP streaking pattern SST2
192 (11 zigzag) produced less single colonies than manual streaking for 6 of the 12
193 inoculum-CFU combinations, thereof 5 significantly ($p<0.001$, Figure 2, B and C). In
194 contrast, WASP streaking pattern SST6 (27 zigzag) and InoqulA (20 zigzag) produced
195 significantly more single colonies than manual streaking for the majority of inoculum-
196 CFU combinations ($p<0.001$, Figure 2, B and C). For 8 out of 12 inoculum/CFU
197 combinations the WASP SST6 streaking pattern produced significantly more single
198 colonies as compared to InoqulA, WASP SST2 or manual streaking ($p<0.001$, Figure 2,
199 B and C).

200 For mixed cultures of *E. coli*, enterococci, and CoNS both WASP SST6 and
201 InoqulA yielded significantly more single colonies as compared to manual streaking
202 ($p<0.001$). No significant difference in the recovery of single colonies was found for
203 mixed inocula when comparing WASP SST6 and InoqulA ($p=0.071$) for the 10 µl
204 inoculum, whereas for the 1 µl inoculum InoqulA BT produced significantly more
205 colonies ($p=0.001$).

206 ***Head to head comparison of clinical samples***

207 To study the performance of the WASP and WASPLab in the routine
208 microbiological work up we evaluated fully automated WASP processing (streaking,
209 incubation and reading) with manual processing for 379 clinical urine samples. Based
210 on the evaluation of optimal inoculation and streaking pattern (see above), a 10 µl

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inoculum combined with SST6 (27 zigzag) streaking pattern was chosen for this evaluation. We found an agreement between automated WASP processing and manual workup for detected morphologies, recovered species, and CFU/ml, in 177 (46.7%), 287 (75.7%), and 239 (63.1%), of all 379 samples. However, WASP yielded significantly higher numbers of morphologies and species recovered as compared to manual processing in 180 (47.5%), and 66 (17.4%) of the 379 samples ($p<0.001$, Table 1, Figure 4, A and B). For 122 (32.2%) of the 379 samples, WASP workup (10 µl inoculum) indicated a higher CFU count/ml than manual handling (mean increase of 1 $\log_{10}$).

To exclude a bias due to the higher inoculum used in WASP processing, as compared to manual processing, a subset of 121 samples were WASP-inoculated using a 1 µl loop. No significant difference in CFU count/ml was detected between automated and manual workup, when inoculum was equally set to 1 µl ($p=0.176$, Table 2, Figure 4 C). However, the percentage of samples which displayed higher numbers of morphologies and higher numbers of recovered species was still significantly higher when using automated sample processing, as compared to manual workup (42/121, i.e. 34.7%, and 18/121, i.e. 14.9% of samples, respectively, $p<0.001$, Table 2, Figure 4 A and B).

Automated processing lead to the detection of more potential pathogens with both the 10 µl and the 1 µl inoculum (3.4% and 9.1% of all 379 and 121 urine samples processed with the corresponding inoculum, respectively, Table 2).

The percentage of urine samples categorized in clinical reports as “positive”, i.e. treatment indicated, or “negative”, i.e. no treatment indicated, did differ but not

234 statistically significantly between manual or automatic handling. Overall, 37.2% and
235 40.4% of 379 samples were categorized as “positive” for manual and automated workup
236 respectively, while 62.8 and 59.6% were categorized as “negative” (Table 1). This ratio
237 was not affected by using different loop sizes for inoculation (compare to Table 2).
238 The significantly higher number of morphologies detected by WASPLab
239 processing lead to significantly more MALDI-TOF based identifications. However, the
240 number of subsequent antibiotic susceptibility tests performed was found not
241 significantly different between automated and manual workup, irrespective of whether
242 inoculation was done using a 10 µl or 1 µl loop (Tables 1 and 2).

Discussion

Evaluation of the optimal inoculum

Traditionally, North American clinical laboratories use a 1 µl inoculum for urine specimens, while European laboratories inoculate 10 µl as the primary inoculum according to various guidelines (8, 11, 12, 17, 18). General arguments between the two inoculation volumes are a potentially decreased sensitivity using a 1 µl inoculum and the missing of pathogens due to a potential lack of single colonies using a 10 µl inoculum for high CFU counts. We aimed at determining the optimal inoculum for the majority of CFU/pathogen combinations that are most frequently encountered in the clinical laboratory. *E. coli* was chosen as the most prevalent uropathogen (1). Enterococci and CoNS were selected to represent the most frequently encountered Gram-positive species in urine specimens (10). On whole plates the 10 µl inoculum was demonstrated to be superior to the 1 µl inoculum in order to maximize the frequency of single colony recovery, particularly for CFUs of $\leq 10^6$/ml. As positivity rates and the number of potential pathogens did not differ between the 1 µl and the 10 µl inoculum, the abovementioned concerns on decreased sensitivity (1 µl inoculum) and missing of pathogens (10 µl inoculum) could not be confirmed. A higher frequency of single colony recovery using automated inoculation may have contributed to the increased detection of potential pathogens (see also “Head to head comparison of clinical samples”). However, the effect of single colony recovery and improved visual inspection by high resolution imaging on sample categorization cannot be distinguished in this study.

Evaluation of the optimal streaking pattern

For pure cultures, WASP SST6 streaking was superior to both WASP SST2 and InoqulA streaking with respect to maximize the recovery of single colonies, independently of the inoculum volume. For mixed cultures, single colony counts generated by WASP SST6 and InoqulA streaking did not differ significantly using a 10 µl inoculum (p=0.071). However, the number of samples investigated was limited, and a larger follow up study may reveal statistically significant results given the borderline p-value. The bench-top InoqulA in combination with manual pipetting produced more colonies as compared to the SST6 for the 1 µl inoculum (p=0.001). However, the fully automated InoqulA cannot handle inoculation volumes lower than 10 µl. In part, these findings are in contrast to a recent study that reported the InoqulA to be superior to WASP streaking with respect to the recovery of single colonies (4, 5, 13). In our study, this effect was shown mainly for exceptionally high CFU counts of 10^7 to 10^8 CFU/ml. However, as the vast majority of clinical specimens (228/306 = 74.5% in this study) contain up to 10^5 CFU/ml. Here, for pure cultures WASP streaking was even superior to the InoqulA method, if SST6 streaking with 27 zigzags was applied. WASP SST2 streaking using 11 zigzags was significantly inferior in generating single colonies. Thus, the critical parameter was the streaking pattern selected, i.e. number of zigzags, rather than the instrument used for automated inoculation. Differences in streaking patterns may be the reason for discrepancies between the results of this study and the results of the studies of Croxatto, Froment, and Mischnik as discussed above (4, 5, 13).

Both WASP SST6 and InoqulA were superior to manual streaking in maximizing single colony recovery. These findings are in agreement with those of other authors (4).

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The same study found a significant improvement of automation over manual processing mainly for high CFU counts (>10^6/ml), the present study demonstrates a significant increase in recovery of single colonies using automated inoculation for CFU counts down to10^4 CFU/ml (4).

Head to head comparison of clinical samples

WASP processing of clinical specimens yielded significantly more morphologies and species recovered as compared to manual processing, independently from the number of CFU counts present in the sample. This finding parallels those of a previous study that analyzed urine specimens processed with the BD-Kiestra system versus manual handling (5, 18). Indeed, next to a higher number of morphologies and species isolated, automated processing by WASP lead to detection of more potential pathogens. Other authors evaluating the BD-Kiestra system with urine specimens did not find more pathogens; however, plate reading was not done by camera but by the unaided eye (18). The high resolution of the WASPLab imaging system may essentially contribute to the higher number of morphologies detected, resulting in a higher number of identified species and pathogens.

The percentage of categorization of urine samples in clinical reports as “positive”, i.e. treatment indicated, or “negative”, i.e. no treatment indicated, did differ but not statistically significant between automated or manual handling. These results are in agreement with data of other studies evaluating the BD-Kiestra system (18).

The results of the head to head comparison of clinical samples demonstrated that automation in urine microbiology is feasible. However, despite a higher number of potential pathogens within “positive” samples in the automated workup, the overall

categorization of samples as positive or negative was not significantly different between automated and manual processing.

A limitation of this study is that a reliable evaluation of the time to result was not possible, because administrative and organizational lab procedures (for instance no 24h/7d service) must be adapted during the process of automated workflow implementation as the influence of these factors on time to result is significant. As the system was primarily evaluated technically, and WASPLab was not part of the diagnostic routine workflow yet, reliable conclusions regarding time to result could not be drawn from this study and should be subject to a follow up work. There are three main conclusions that can be drawn from the present study: i) The streaking pattern, in particular the number of zigzags/length of streaking lines is of critical importance for increasing the number of single colonies recovered from primary cultures; ii) Automated streaking by WASP can significantly increase the number of single colonies recovered, iii) Automated WASPLab processing results in a higher number of detected morphologies, species, and pathogens. In summary, our findings demonstrate that automated sample processing by WASPLab is going to improve the quality of urine microbiological analysis.

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395

Figures

Figure 1. Study design and evaluation steps of part 1 the evaluation of the optimal inoculation volume and streaking pattern (A) and part 2 the head to head comparison (B).

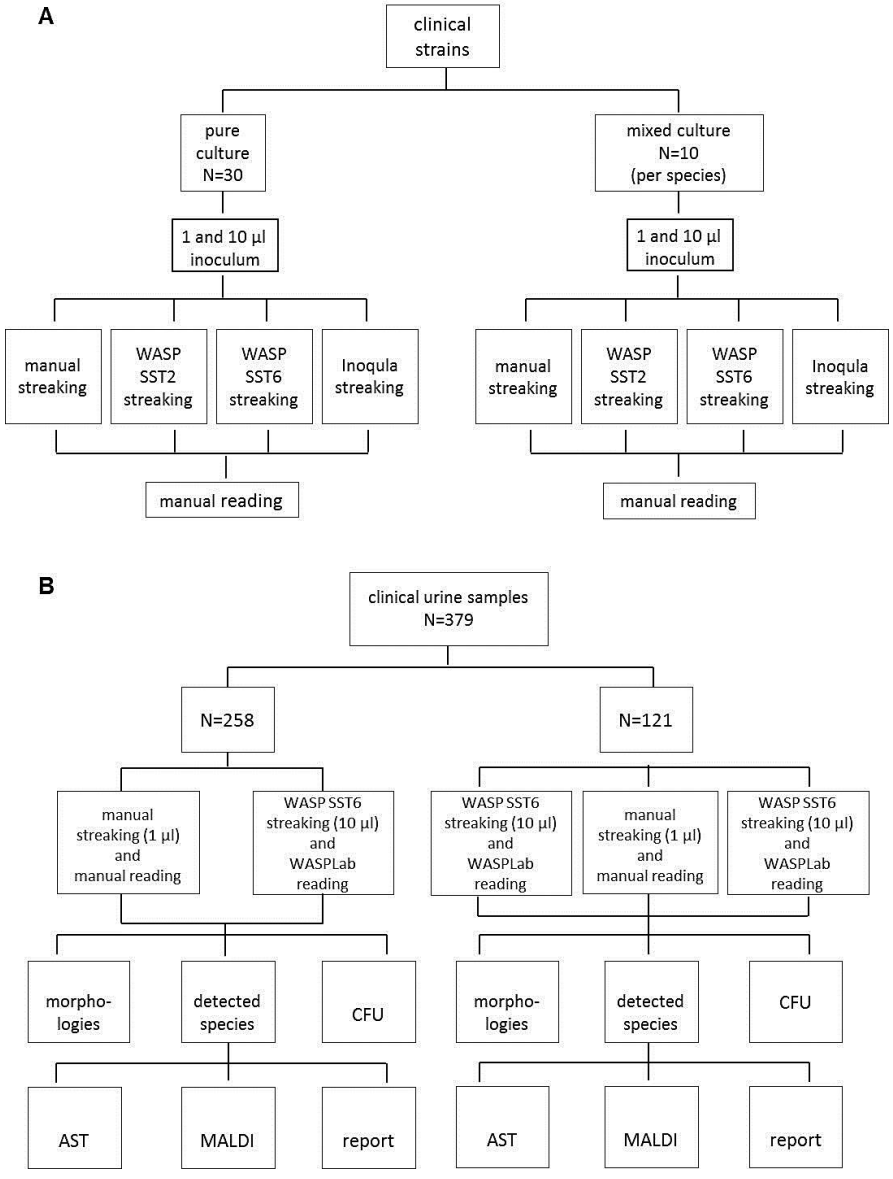


Figure 2. Streaking pattern details and resulting numbers of single colony counts. (A) One manual (routine) and three automated quantitative streaking patterns with varying numbers of zigzag (zz) lines shown in brackets; WASP single streak type 2 (SST2); WASP single streak type 6 (SST6) and InoqulA. Comparison of single colonies obtained by manual and automated streaking. 1 µl and 10 µl *E. coli* (B) and enterococci (C) bacterial suspensions were used with CUFs ranging from 10^4 to 10^6. The mean values of 30 clinical strains per species are shown with their standard deviation.

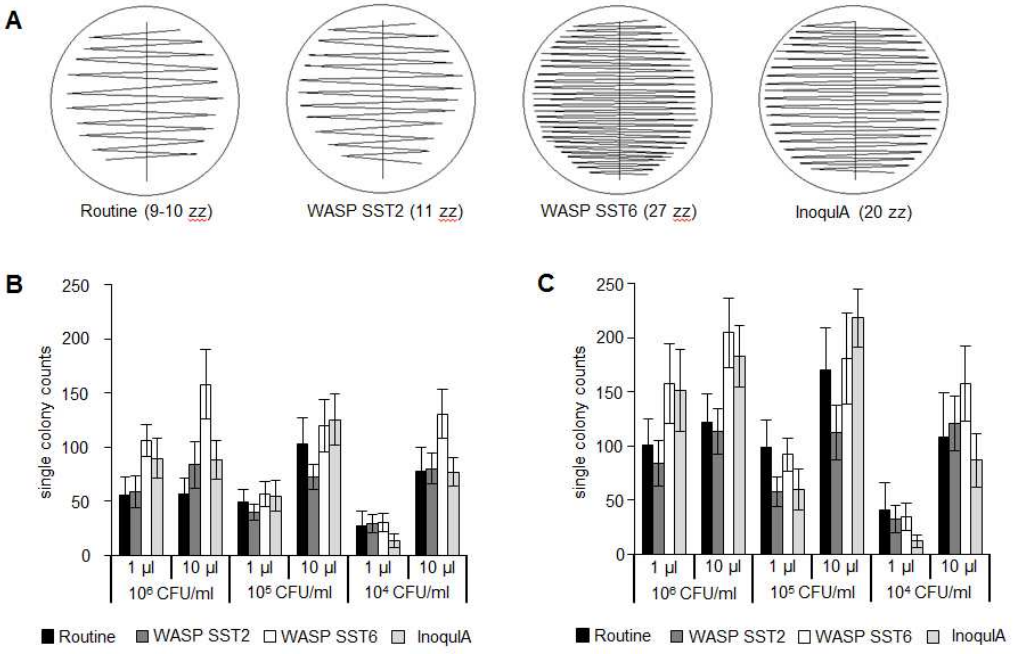
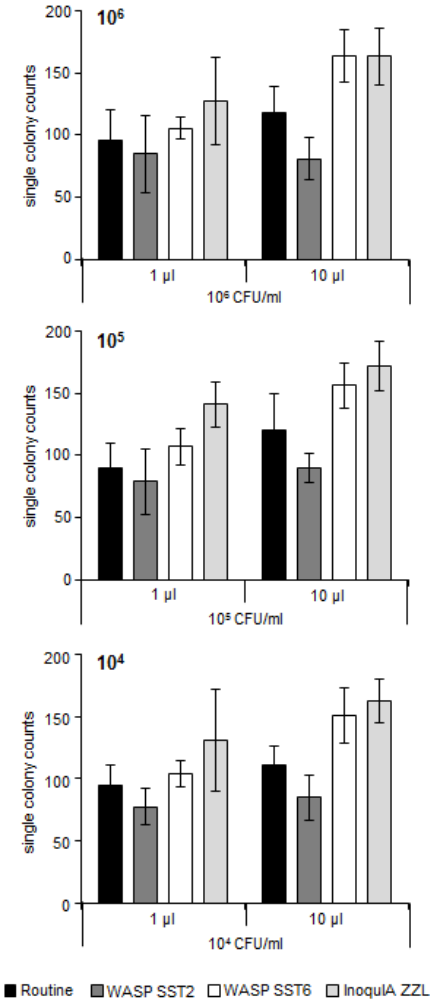


Figure 3 Cumulated numbers of single colonies recovered from mixed cultures containing variable CFU counts of *E. coli* (10^4 to 10^6 per ml as indicated in the Figure) PLUS fixed CFU counts of 10^6 per ml of both enterococci and coagulase negative staphylococci. Mean values of ten mixed cultures prepared with individual clinical strains are shown with the according standard deviation.



418 **Figure 4** Correlation of morphologies (A), recovered species (B), and CFU resulting (C)
419 from the head to head comparison of 121 and 379 clinical samples, respectively. Data
420 indicate a shift to higher numbers for all three parameters for automated as compared to
421 manual inoculation.
422

A Morphology Correlation

WASP 1µl / Manual	0	1	2	3	4	≥5
0	37	1	1			
1	1	12	11	1		
2			5	4	2	4
3			3	9	6	3
4				1	5	9
≥5					3	3

WASP 10µl / Manual	0	1	2	3	4	≥5
0	73	29	10	2		
1		30	30	8		1
2		1	18	18	13	6
3		1	5	24	29	13
4				6	19	21
≥5				2	7	13

B Recovered species correlation

WASP 1µl / Manual	0	1	2	3	4	≥5
0	55	8	4			
1	1	33	6			
2		5	6			
3		1	1	1		
4						
≥5						

WASP 10µl / Manual	0	1	2	3	4	≥5
0	161	35	5			
1	8	91	24	1		
2	4	9	30		1	
3		1	3	5		
4						
≥5				1		

C CFU correlation

WASP 1µl / Manual	n. g.	< 10^4	10^4	10^5	10^6	≥10^6
n. g.	37	2				
< 10^4	1	17	8		1	
10^4		4	14	2		
10^5			1	12	4	
10^6				3	15	
≥10^6						

WASP 10µl / Manual	n. g.	< 10^4	10^4	10^5	10^6	≥10^6
n. g.	73	40	1			
< 10^4		74	18	6	1	
10^4		11	30	19	7	
10^5		2	1	22	30	
10^6				4	40	
≥10^6						

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Table 1. Results of the head to head comparison of clinical samples. Manual inoculation versus WASP inoculation (10 µl loop). Significant differences are indicated in bold (non-parametric Wilcoxon signed rank test ($p<0.05$) and crosstab chi-square test of independence ($p<0.05$).

	N	Samples with indicated parameter (N, % of all samples)					
Parameter		**Manual**	**WASP**	**Identical**	**Manual > WASP**	**WASP > Manual**	**p**
Total number of samples	379						
Morphologies				177 (46.7%)	**22 (5.8%)**	**180 (47.5%)**	0.000
Colony forming units (CFU) /ml				239 (63.1%)	**14 (4.8%)**	**122 (32.2%)**	0.000
Recovered species				287 (75.7%)	**26 (6.9%)**	**66 (17.4%)**	0.000
Total No. of MALDI-TOF identifications		**253**	**313**				0.000
Total No. of susceptibility tests		149	163				0.337
Report				199 (52.5%)	180 (47.5%)		
Positive result		141 (37.2%)	153 (40.4%)				
Negative result		238 (62.8%)	226 (59.6%)				
Possible Pathogens[1)]		159 (42%)	172 (45.4%)				
Contaminated		10 (2.6%)	10 (2.6%)				

[1)] Possible Pathogens: Gram negative rods, *Staphylococcus aureus, Staphylococcus lugdunensis, Staphylococcus saprophyticus, Streptococcus group* B, C or G, enterococci, yeasts, *Corynebacterium glucuronolyticum, Corynebacterium urealyticum*

Table 2. Results of the head to head comparison of clinical samples. Manual inoculation versus WASP inoculation (1 µl loop). Significant differences are indicated in bold (non-parametric Wilcoxon signed rank test ($p<0.05$) and crosstab chi-square test of independence ($p<0.05$).

	N	Samples with indicated parameter (N, % of all samples)					
Parameter		**Manual**	**WASP**	**Identical**	**Manual > WASP**	**WASP > Manual**	**p**
Total number of samples	121						
Morphologies				71 (58.7%)	**8 (6.6%)**	**42 (34.7%)**	0.000
Colony forming units (CFU) /ml				95 (78.5%)	9 (7.4%)	17 (14.1%)	0.176
Recovered species				95 (78.5%)	**8 (6.6%)**	**18 (14.9%)**	0.043
Total No. of MALDI-TOF identifications		**76**	**100**				0.001
Total No. of susceptibility tests		47	52				0.601
Report				79 (65.3%)	42 (34.7%)		
Positive result		47 (39.7%)	51(42.1%)				
Negative result		73 (60.3%)	70 (57.9%)				
Possible pathogens [1)]		48 (39.7%)	59 (48.8%)				
Contaminated		6 (5%)	2 (1.7%)				

[1)] Possible Pathogens: Gram negative rods, *Staphylococcus aureus, Staphylococcus lugdunensis, Staphylococcus saprophyticus, Streptococcus group* B, C or G, enterococci, yeasts, *Corynebacterium glucuronolyticum, Corynebacterium urealyticum*